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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2788.18 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-6
Perfect score: 1083
Sequence: 1 atgaagctccttaccatgc.....ctggctgttcaagaataa 1083

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl.*
1: gb_ha:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
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37: em_hg_vrt:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225.4	20.8	808	3 AB045178	AB045178 Reticulit
2	224.8	20.8	840	3 AB045172	AB045172 Reticulit
3	218.2	20.1	1443	8 FSOKCH	AB045172 Reticulit
4	218.2	20.1	1473	6 A21795	AB045172 Reticulit
5	218.2	20.1	1473	6 A23637	AB045172 Reticulit
6	218.2	20.1	1473	6 A23646	AB045172 Reticulit
7	218.2	20.1	1473	6 A23955	AB045172 Reticulit
8	218.2	20.1	1473	6 A23959	AB045172 Reticulit
9	218.2	20.1	1473	6 A41660	AB045172 Reticulit
10	218.2	20.1	1473	6 AR072922	AB045172 Reticulit
11	218.2	20.1	1473	6 BD002249	AB045172 Reticulit
12	218.2	20.1	1473	6 BD010853	AB045172 Reticulit
13	218.2	20.1	1473	6 I13885	AB045172 Reticulit
14	218.2	20.1	1473	6 I21317	AB045172 Reticulit
15	218.2	20.1	1473	6 I57984	AB045172 Reticulit
16	214.4	19.8	784	3 AB045167	AB045167 Reticulit
17	213.8	19.7	781	3 AB045165	AB045165 Reticulit
18	212.8	19.6	780	3 AB045168	AB045168 Reticulit
19	212.8	19.6	785	3 AB045169	AB045169 Reticulit
20	208.8	19.3	774	3 AB045170	AB045170 Reticulit
21	208.8	19.3	828	3 AB045171	AB045171 Reticulit
22	206.4	19.1	710	3 AB045171	AB045171 Reticulit
23	205.4	19.0	1423	6 AR094309	AB045171 Reticulit
24	198.4	18.3	783	3 AB045173	AB045173 Reticulit
25	198.2	18.3	761	3 AB045175	AB045175 Reticulit
26	195	18.0	924	6 A68074	AB045175 Reticulit
27	195	18.0	924	6 A68074	AB045175 Reticulit
28	192	17.7	798	3 AB045166	AB045166 Reticulit
29	187.2	17.3	785	3 AB045177	AB045177 Reticulit
30	187.2	17.3	802	3 AB045176	AB045176 Reticulit
31	185.6	17.1	759	3 AB045174	AB045174 Reticulit
32	184.4	17.0	919	6 A68072	AB045174 Reticulit
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36	181	16.7	1174	6 A92311	AB045174 Reticulit
37	181	16.7	1174	6 AR075389	AB045174 Reticulit
38	181	16.7	1174	6 AR094310	AB045174 Reticulit
39	178.2	16.5	927	6 AR094307	AB045174 Reticulit
40	178	16.4	960	6 AR094305	AB045174 Reticulit
41	177	16.3	894	6 AR094306	AB045174 Reticulit
42	170.2	15.7	913	6 AR094311	AB045174 Reticulit
43	169.4	15.5	885	6 AR094316	AB045174 Reticulit
44	161.8	14.9	1057	6 BD002248	AB045174 Reticulit
45	161.8	14.9	1060	6 A21793	AB045174 Reticulit

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Reticulitermes speratus hindgut symbiont 130484 CNA to mRNA, linear INV 14-FEB-2001
ACCESSION AB045178
VERSION
KEYWORDS
SOURCE
ORGANISM Reticulitermes speratus hindgut symbiont 130484
REFERENCE
AUTHORS
TITLE
Diverse genes of cellulase homologues of glycosyl hydrolase family

Db	310	GGAGGCGAAACGGGCGCTGTGTGCAATTGCTATGAGCTTACCTTACACAGTGGCCAGTT	369
Qy	754	AAGGTAAGAAGATGCTGTCTTCAAGTAAACAACACTGCTTGTGACTTGGCTTAACT	813
Db	370	AATGAAAGAAATGCTGTCTTCAAGTAAACAACCGGTGTGATCTTGGTTCAA----	425
Qy	814	GGTGCTCACTTGACTTGCAAAATGCGCGGTGTGATGTGTGATCTTCAATGATGTGGCC	873
Db	426	-----TCAATTGATCTTGCATTTCCCGAGAGAGGTGTGGAAATTTTACATGATGACT	480
Qy	874	ACTCAATGGGATGCTCCACCGATGATGTGTGGGTGCAAGATACAGCGGCTGTCTTGTGCC	933
Db	481	CAACATACAGGGGGCGCCCTCCGATGATGATGGGGAAGCGATATGGTGGTGTCACTTCTGA	540
Qy	934	TCTGACTGTTTCAACTTCTTCTTGTGCCCTTCAAGCTGTTGTAAATGAGATTCGGCTGG	993
Db	541	TCTGAATGTTCTCAGCTTCCATCAGTCTTTCAGGCTGATCCAGTGAACATTTGATTTGG	600
Qy	994	TTCAAAAACGCTGATTAACCCAAACATGACCTTAAACAAGTTACTGTCCCAAGGCTATC	1053
Db	601	TTCCAAAATGCTGACAAACCTTCAATCAATTTCAATCAAGTACCTGCCCCAAGATTTG	660
Qy	1054	ACTGCCAAGTCTGGCTGTTCAAAGAAATTA	1083
Db	661	ACAGCAAAACCAATTCGACAGCACTTAA	690
RESULT 3			
FSOCH			
LOCUS	FSOCH	1443 bp	mRNA
DEFINITION	Fusarium oxysporum K-family cellulase homologue mRNA, complete cds.		
ACCESSION	L29381		
VERSION	L29381.1	GI:520822	
KEYWORDS	K-family cellulase homologue; cellulase; homologue.		
SOURCE	Fusarium oxysporum CDNA to mRNA.		
ORGANISM	Fusarium oxysporum		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.		
REFERENCE	1 (bases 1 to 1443)		
AUTHORS	Sheppard, P.O., Grant, F.J., Oort, P.J., Sprecher, C.A., Foster, D.C., Hagen, F.S., Ushall, A., McKnight, G.L. and O'Hara, P.J.		
TITLE	The use of conserved cellulase family-specific sequences to clone cellulase homologue cDNAs from Fusarium oxysporum		
JOURNAL	Gene 150 (1), 163-167 (1994)		
MEDLINE	95047531		
PUBMED	7959045		
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CDS			
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ORIGIN			
Query Match	20.1%	Score 218.2;	DB 8; Length 1443;
Best Local Similarity	63.0%	Pred. No. 1e-48;	
Matches	394; Conservative	0; Mismatches 213;	Indels 18; Gaps 3;
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Db	129	GTGTGCTCTTTCGGAAGGGGCTCACTCTACCTGATCTACTGGAATTCGGAATTCGCAAGCCTTTCGT	188
Qy	509	GTTTGAGCCCGGTAAAGGCTGATGTCACTTCCTCCCTGTTGGCTCTGTATACAGAGATGTAAGA	568
Db	189	CTTGAGACCGGAAGGGCTGTCTCAACCCCTCTGCTTTAACTGTGATTAAGAACACAACC	248
Qy	569	CTCTTGCTGATTAACAACACTCAAAAGGAGCTGT---GTTGGTGAGAGCAGCTACACCTGTA	625
Db	249	CCATTTCCAAACCAACATGCTGTCAACGATTTGTAGAGGTGTGTGTTCTGTCTTATGCTTGCA	308
Qy	626	ATGACAAATCAACCTTGGGTTGTTAGCCAGCAACCTTGCCTACGATTTTGCCCGCTCTTCCA	685
Db	309	CCAACTACTCTCCCTGGGCTGTCAACGATAGAGCTTGCTCAAGTTTGGCTGTACCAAGA	368
Qy	686	TTTCTGTGTGTAAGCAAGCTACTTGTGTGTGTGTGCTGTTCGAACTACATTCACCTGTA	745
Db	369	TCTCCGGTGTGCTCGAAGGCCAGCTGTGTGTGTGTGTCTTGAATGCTTTCACCTTCACACTG	428
Qy	746	CTGCGCTCAAGGGTAAAGATGTTTTCAGATACCAACACCTGTCTTCACTTGGCT	805
Db	429	GCCCCGTCAAGGGGGAAGATGATGTCTCAAGTCCACCAACACTGGAAGTATCTCGGCG	488
Qy	806	CTAACACTGAGCTCACTTTGACTTTGCAAAATGCCCGGTGTGTGTGTGTATTAACAATG	865
Db	489	ACAAAC-----CACTTGATCTTCATGATGCCCGGCGGTGTGTGTGTATCTTTCAGAC	539
Qy	866	GTTGTGCACTCAATGAGGGGTCTCCCAACGATGTTGGGTGCAAGATACGCGGCTGTT	925
Db	540	GCTCACCCTCTGATGTCG-----CAAGGCTCTCGGGGGGTGCCAGTACGGCGGATCT	593
Qy	926	CTTCTGCTCTGATCTGTTCTTCACTTCTTCTTCTGCTTCAAGCTGTGTGTATAGTGAAT	985
Db	594	CTTCCCGAAGGAATGATAGTACATCCCGAGCTTCTCAAGACGTTTGCACATGGCGAT	653
Qy	986	TCGGCTGATTCAAAAAGCTGATTAACCCCAACATGACATGACCAAAAGTAACTGTCCCA	1045
Db	654	TCGACTGTTGAGAAAGCCGACCAACCTGACTTCACTTTGAGCAGGTTCAAGTCCCA	713
Qy	1046	AGGCTATCACTGCCAAGTCTGGCTG	1070
Db	714	AGGCTCTCTCGACATCATGTGATG	738
RESULT 4			
A21795		1473 bp	linear
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
FEATURES			
source			
CDS			
BASE COUNT			

ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

449 GTGGTCCCTCGGTAATGTTGAACCACTCGTACTGAGATGTTGTAAGCCCTTCTTCA 508
 143 GTGCTGCTTCTGGAAGGGCTCACTACTGATGATGAGATGCTCAAGCCCTTCTTCT 202
 509 GTTGGCCCGTAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 568
 203 CTGGAGCGGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 262
 569 CTCTGCTGATTAACAACCTCAAAAGGCTG---GTGGTGGTGAAGCTCACTACTGTA 625
 263 CCAATTCCAAACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 322
 626 ATGACAACTCAACCTTGGCTGTTAGGAGACCTTGGCTGATGATGATGATGATGATG 685
 323 CCAACTGCTCTCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 382
 686 TTTCTGGTGGTGAAGGCTACTGTTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG 745
 383 TCTCGGTTGGCTCGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 442
 746 CTGGCTGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 805
 443 GCCCGCTCAAGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 502
 806 CTAACTGCTGCTCACTTGAATGATGATGATGATGATGATGATGATGATGATGATG 865
 503 ACAAC-----CACTGATGATGATGATGATGATGATGATGATGATGATGATG 553
 866 GTTGGTCACTCAATGAGGCTGCTCCACGATGATGATGATGATGATGATGATGATG 925
 554 GCTGACCTCTGAGTGG-----CAAGGCTCTGGGGGCTGCGGATGATGATGATGAT 607
 926 CTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 985
 608 CTCCGGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
 986 TGGGCTGTTCAAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1045
 668 TGAAGTGGTGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 727
 1046 AGGCTATCACTGCGAAGTCTGCTG 1070
 728 AGGCTCTCTCGACATCAAGTGAATG 752

RESULT 5
 A23637 1473 bp mRNA linear PAT 1b-SEP-1995
 LOCUS F. oxysporum endoglucanase gene.
 DEFINITION A23637.1 GI:832888
 ACCESSION endoglucanase.
 VERSION Fusarium oxysporum.
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS 1 (baees 1 to 1473)
 TITLE Convents,A.C., Busch,A. and Baeck,A.C.
 JOURNAL Detergent compositions with high activity cellulase and softening
 PATENT EP 0495258-A 3 22-JUL-1992;
 KEYWORDS THE PROCTER & GAMBLE COMPANY
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CDS

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BASE COUNT 343 a 453 c 337 g 340 t
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Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

449 GTGGTCCCTCGGTAATGTTGAACCACTCGTACTGAGATGTTGTAAGCCCTTCTTCA 508
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 509 GTTGGCCCGTAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 568
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 626 ATGACAACTCAACCTTGGCTGTTAGGAGACCTTGGCTGATGATGATGATGATGATG 685
 323 CCAACTGCTCTCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 382
 686 TTTCTGGTGGTGAAGGCTACTGTTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG 745
 383 TCTCGGTTGGCTCGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 442
 746 CTGGCTGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 805
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 806 CTAACTGCTGCTCACTTGAATGATGATGATGATGATGATGATGATGATGATGATG 865
 503 ACAAC-----CACTGATGATGATGATGATGATGATGATGATGATGATGATG 553
 866 GTTGGTCACTCAATGAGGCTGCTCCACGATGATGATGATGATGATGATGATGATG 925
 554 GCTGACCTCTGAGTGG-----CAAGGCTCTGGGGGCTGCGGATGATGATGATGAT 607
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 986 TGGGCTGTTCAAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1045
 668 TGAAGTGGTGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 727
 1046 AGGCTATCACTGCGAAGTCTGCTG 1070
 728 AGGCTCTCTCGACATCAAGTGAATG 752

RESULT 6
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 LOCUS F. oxysporum endoglucanase gene.
 DEFINITION A23646
 ACCESSION A23646.1 GI:832892
 VERSION Fusarium oxysporum.
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 1473)
AUTHORS Convent, A.C., Busch, A. and Baek, A.C.
TITLE Detergent compositions with high activity cellulase and quaternary ammonium compounds
JOURNAL Patent: EP 0495554-A 3 22-JUL-1992;
THE PROCTER & GAMBLE COMPANY
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CKRDDSSFPAPKVDTSASRQPSASAKTISAALAAQPOKTKDSAPVOKSSTKPPA
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BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;
QY 449 GTGTCCTCCGGTATGTAAGCAACACTCGCTATCGGAGATTGTTGAAGCTTTTGA 508
DB 143 GTGTCCTTCGGAAGCGGTCACTCTACATACGGAATTCGCAAGCTTCTTGCT 202
QY 509 GTTGCCCGGTAAGCTGATGTCACCTCCCGTGTGGCTCCGTAACAAGATGTTAGA 568
DB 203 CTTGAGCGGAAGGCTGCTGCAAGCGCCCTGCTTTAACTTGTATGAACGACCAACC 262
QY 569 CTCCTGCTGATTAACAACACTCAAAACGGCTGT---GTTGGTGATGACAGTACACTGTA 625
DB 263 CCAATTTCCAAACCAATGCTGCAACGGTTGAGAGGGTGTGTCTGCTTATGTTGCA 322
QY 626 ATGACATCAACCTTGGGTTGTAAGCAAGACTTGCCTTAAGGTTTCCCGCTGTTCCA 685
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QY 686 TTTCTGGGTGTAAGCAAGCTACTGTTGTTGGCTGTTTGGAACTGCAATTCACCTCTTA 745
DB 383 TCTCCGGGTGCTCCAGGCTCAGCTGTGCTGTGCTGTGATGCTTTGACTTTCACCACTG 442
QY 746 CTGCGTCAAGGGTAAAGATGTTGTTCAAGTAAACAACCTGTTCTGACCTTGCT 805
DB 443 GCCCGTCAAGGGCAAGAAATGATGTCAGTCCACCAACACTGGAAGTATCTCGGCG 502
QY 806 CTAACACTGCTGCTGCTTGAATGCAATGCTCCGGTGTGTGTGTTGATCTAACAATG 865
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QY 866 GTTGGGCACTCAATGAGGATGCTCCACGATGTTGGGGTGAAGATTAAGCGGCTGTTT 925
DB 554 GCTGACCTCTGAGTTGCG-----CAAGGCTCTGGGGGTGCGCAAGTACGGCGGTATCT 607
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QY 1046 AGGCTATCACTGCCAAGCTGCTG 1070
DB 728 AGGCTCTCCGACATCATGATGATG 752
RESULT 7
A23955
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DEFINITION A23955
VERSION A23955.1 GI:832896
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 1473)
AUTHORS Baek, A.C., Busch, A. and Ceulemans, R.A.A.
TITLE Compact detergent compositions with high activity cellulase
JOURNAL Patent: EP 0495257-A 3 22-JUL-1992;
THE PROCTER & GAMBLE COMPANY
FEATURES Location/Qualifiers
source 1. 1473
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BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;
QY 449 GTGTCCTCCGGTATGTAAGCAACACTCGCTATCGGAGATTGTTGAAGCTTTTGA 508
DB 143 GTGTCCTTCGGAAGCGGTCACTCTACATACGGAATTCGCAAGCTTCTTGCT 202
QY 509 GTTGCCCGGTAAGCTGATGTCACCTCCCGTGTGGCTCCGTAACAAGATGTTAGA 568
DB 203 CTTGAGCGGAAGGCTGCTGCAAGCGCCCTGCTTTAACTTGTATGAACGACCAACC 262
QY 569 CTCCTGCTGATTAACAACACTCAAAACGGCTGT---GTTGGTGATGACAGTACACTGTA 625
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QY 626 ATGACATCAACCTTGGGTTGTAAGCAAGACTTGCCTTAAGGTTTCCCGCTGTTCCA 685
DB 323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTTAAGGTTTCCGCTGACCAAGA 382
QY 686 TTTCTGGGTGTAAGCAAGCTACTGTTGTTGGCTGTTTGGAACTGCAATTCACCTCTTA 745
DB 383 TCTCCGGGTGCTCCAGGCTCAGCTGTGCTGTGCTGTGATGCTTTGACTTTCACCACTG 442
QY 746 CTGCGTCAAGGGTAAAGATGTTGTTCAAGTAAACAACACTGTTCTGACCTTGCT 805
DB 443 GCCCGTCAAGGGCAAGAAATGATGTCAGTCCACCAACACTGGAAGTATCTCGGCG 502
QY 806 CTAACACTGCTGCTGCTTGAATGCAATGCTCCGGTGTGTGTGTTGATCTAACAATG 865
DB 503 ACAAC-----CACTTCGATCTCATGATGCTCCGGGCTGTGTGCTGCTGACG 553

QY 866 GTTGTGCACTGATGGGAGTGTCCACGATGTTGGGATGCAAGATACGGCGGTGTT 925
 DB 554 GGTGACCTCTGATGTTGG-----CAAGCTCTGGGAGTGGCCGATGACGGCGGTATCT 607
 QY 926 CTCTGCTCTGATGTTGTTAACTCTTCTTCTGCTTCTTCAAGCTGTTGTAAGGAGAT 985
 DB 608 CTTCCGGAAGCGAATGTGATGATGATCCCGAGCTTCTCAAGAGCGTTGCCACTGGGAT 667
 QY 986 TGGCTGCTGTTCAAAACGCTGATTAACCCAGCATGACCTACAAACAGTTACTGTCCCA 1045
 DB 668 TCGACTGTTGCAAGACCGACACCTGATCTTCACTTTGAGCAGGTGATGGCCCCA 727
 QY 1046 AGGCTATCACTGCGCAAGTCTGCTG 1070
 DB 728 AGGCTCTCTCGACATCAGTGATG 752

RESULT 8
 A23959 1473 bp DNA linear PAT 01-MAR-1995
 LOCUS Endoglucanase gene.
 ACCESSION A23959
 VERSION A23959.1 GI:832900
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.

REFERENCE 1 (bases 1 to 1473)
 AUTHORS McCordqudale, F. and Busch, A.
 TITLE Dye transfer inhibiting compositions
 JOURNAL Patent: EP 0540784-A 3 12-MAY-1993;
 THE PROCTER & GAMBLE COMPANY
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 ALVGAOYGEISRSBESDYSPELLKDGCHMRPDMFNANPDFTFEOYQCPALDLSG
 CKRDDSSFPARVDLSASKPQSSSAKTTSSAAAPORTKDSAPVVOKSSTRPAA
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 SVVPAYOCGSGSKAVPNGNLACATGSKCKVKNERYISQCVEN"

CDS
 BASE COUNT 343 a 453 c 337 g 340 t
 ORIGIN
 Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

QY 449 GTGTGCTCCGGTAATGTAAGCACTGCTACTGAGATTGTTGAAGCTTTTGCA 508
 DB 143 GTGTGCTCTTGGAAAGCGTCACTGATGATGCGATGCTCAAGCCTTCTGTCT 202
 QY 509 GTTGGCCCGTAAGGCTGATGTCACTCCCTGTTGGCTCCCTTAACAAGAGATGTAAGA 568
 DB 203 CTTGGAAGCGAAAGGCTGTGTCAACGCCCTGCTTTAACTTGTGATTAAGAAAGATACC 262
 QY 569 CTCTTGTGATTAACAACACTCAAAACGCTGT---GTTGTGTAGACGCTACACCTGTA 625
 DB 263 CCAATTTCAACAACAATGCTGTCAACGTTGTGAGGTGTGTTGCTTATAGCTTGCA 322
 QY 626 ATGACATCAACTTGTGTTGTTAGCGACGACTTGTCTTACGTTTCCGCGCTGTTCA 685
 DB 323 CCAACTACTCTCTCGGCGTGTCAACGATGAGCTTGTGCTTACGCTTGTGCTTACCAAGA 382

QY 686 TTTCTGTGTAGAGCAAGCTACTGTGTGTGTGCTGTTTCAACTCACTTCACTCTTA 745
 DB 383 TCTCCGGTGGTCCGAGGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 442
 QY 746 CTGCGCTCAAGGATTAAGATGTTGTTTCAAGTAACCAACTGTTTCACTTGGCT 805
 DB 443 GCCCGGTCAAGGGCAAGATGATTCGTCAGTCACCAACACTGAGAGGATCTCGGCG 502
 QY 806 CTAACTGAGTGTCTACTTGTGTAATGCAATGCTCGGTGTGTGTGTGTGTGTGTGTGTGT 865
 DB 503 AACAC-----CACTTCATCTCATGATGCTCGGCGGTGTGTGTGTGTGTGTGTGTGTGT 553
 QY 866 GTTGTGCACTAATGGGTGTGTCTCCACGATGTTGGGAGTGAAGATACGGCGGTGTT 925
 DB 554 GTGCACTCTGATGTTGG-----CAAGCTCTGGGAGTGGCCGATGACGGCGGTATCT 607
 QY 926 CTCTGCTCTGATGTTTCTAACTTCTTCTTCTGCTTCTTCAAGCTGTTTGAAGGAGAT 985
 DB 608 CTTCCGGAAGCGAATGTGATGATGATCCCGAGCTTCTCAAGAGCGTTGCCACTGGGAT 667
 QY 986 TGGCTGCTGTTCAAAACGCTGATTAACCCAGCATGACCTACAAACAGTTACTGTCCCA 1045
 DB 668 TCGACTGTTGCAAGACCGACACCTGATCTTCACTTTGAGCAGGTGATGGCCCCA 727
 QY 1046 AGGCTATCACTGCGCAAGTCTGCTG 1070
 DB 728 AGGCTCTCTCGACATCAGTGATG 752

RESULT 9
 A41660 1473 bp DNA linear PAT 05-MAR-1997
 LOCUS Sequence 3 from Patent EP0633311.
 ACCESSION A41660
 VERSION A41660.1 GI:2297285
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 unclassified.

REFERENCE 1 (bases 1 to 1473)
 AUTHORS Herboots, I. M. and Jensen, M. P.
 TITLE Hydrophobic amines for cellulase stabilization in liquid detergent
 JOURNAL Compositions containing anionic surfactant and cellulase
 Patent: EP 0633311-A 3 11-JAN-1995;
 PROCTER & GAMBLE (US)
 COMMENT Other publication CA 2165771 950105.
 FEATURES
 source Location/Qualifiers
 1. 1473
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 343 a 453 c 337 g 340 t
 ORIGIN
 Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

QY 449 GTGTGCTCCGGTAATGTAAGCACTGCTACTGAGATTGTTGAAGCTTTTGCA 508
 DB 143 GTGTGCTCTTGGAAAGCGTCACTGATGATGCGATGCTCAAGCCTTCTGTCT 202
 QY 509 GTTGGCCCGTAAGGCTGATGTCACTCCCTGTTGGCTCCCTTAACAAGAGATGTAAGA 568
 DB 203 CTTGGAAGCGAAAGGCTGTGTCAACGCCCTGCTTTAACTTGTGATTAAGAAAGATACC 262
 QY 569 CTCTTGTGATTAACAACACTCAAAACGCTGT---GTTGTGTAGACGCTACACCTGTA 625
 DB 263 CCAATTTCAACAACAATGCTGTCAACGTTGTGAGGTGTGTTGCTTATAGCTTGCA 322
 QY 626 ATGACATCAACTTGTGTTGTTAGCGACGACTTGTCTTACGTTTCCGCGCTGTTCA 685
 DB 323 CCAACTACTCTCTCGGCGTGTCAACGATGAGCTTGTGCTTACGCTTGTGCTTACCAAGA 382

OY	686	TTTCTGGGNGTAGCGAAGCTACTTGGGNTGTGTGCTGTTTGAACTCAATTCAAGCTCTA	745
Db	383	TCTCCGGTGGCTCCGAGGCGACGTGGTGTCTGTGTGTATGCTTTGACCTTCCACACTG	442
OY	746	CTGCCGTCAAGGGTAAAGATGGTGTGTTCAAGTAAACCACTAGTGTCTGACCTTGGCT	805
Db	443	GCCCCGTAAAGGGCAAGAGATGATGTGTCTCACTCAGTCCACCAACTGTGAGATATCTCGCG	502
OY	806	CTAACACTGGTGTCTCATCTTTGACTTTGCAATGCCGGGTGGTGGTGGTATCTTACAATG	865
Db	503	ACAAC-----CACTTCGATCTCATGATGCGCGGGGTGGTGTGCGATCTTCGACG	553
OY	866	GTTGTGGCCACTCATTANGGGGTGTCTCCCAACGATGGTGGGGGTGCAAGATACGGCGGTCTT	925
Db	554	GCTGACCTCTGAGTTCGG-----CAAGGCTCTCGGGGTGACCCAGTAGCGCGGTATCT	607
OY	926	CTTTCGCTCTGACTGTCTTAACCTTCTCTTCTGCGCCTTCAAGCTGGTGTGAATGGAGAT	985
Db	608	CCTCCCGAAGGGAATGTGATAGCTACCCCGAGCTTCTCAAGACGGTTGGCCACTGGCGAT	667
OY	986	TCGGCTGTTCAAAAACGCTGATTAACCAACCATGACCTTACAAACAGATTACCTGTGCCA	1045
Db	668	TCGACTGGTTCGAGAACCGCCGACCACTGACTTACCTTTGAGCAGGTTCAAGTCCCA	727
OY	1046	AGGCTATCACTGCCAAGTCTGGCTG	1070
Db	728	AGGCTCTCTCGACATCAAGTGATG	752

LOCUS	AR072922	1473 bp	DNA	linear	PAT 28-AUG-2000
DEFINITION	Sequence 3 from patent US 5948672.				
ACCESSION	AR072922				
VERSION	AR072922.1	GI:999685			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassefied.				
AUTHORS	1 (baes I to 1473)				
TITLE	Rasmussen, G., Mikkelsen, J., Moshaleh, M., Packard, S., Anant, H., Hagen, F., Hjort, C., Mølland, A., and Hestrup, S. Cellulase preparation comprising an endoglucanase enzyme Patent: US 5948672-A 3 07-SEP-1999;				
JOURNAL	Location/Qualifiers				
FEATURES	1..1473				
source	/organism="unknown"				
BASE COUNT	343 a	453 c	337 g	340 t	
ORIGIN					
Query Match	20.1%; Score 218.2; DB 6; length 1473;				
Best Local Similarity	63.0%; Pred. No. 1e-48;				
Matches	394; conservative	0; mismatches	213; indels	18; gaps	3;
QY	449	GTGTCCTCCGGATATGATGTAACCACTGCTACTGGAGTTGTGTAGCCTTCTTCA	508		
DB	143	GTGTCCTTCTGGAAACCGCTCACTTACTCGATCTAGCGGATTGTGCAAGCCTTCTTCT	202		
QY	509	GTTGGCCCGGTAAAGGCTGATGCACCTCCCGTTGGGCTCCGTAAAGAGATGTGTAAGA	568		
DB	203	CTTGGAGCGGAAGAGCTGTCTGCAACGCCCTTCTTAACTTGTATTAAGACGCAACC	262		
QY	569	CTTTGTGATTAACAACACTCAAAACGGCTGT--GTTGGTGTGACAGCTTACACTGTGA	625		
DB	263	CCATTTCACAACCAATGCTGTGCAACGGTGTGAGGAGTGAGTTCCTGCTTATGCTTGCA	322		
QY	626	ATGACAATCAACCTTGGGTTGTGTAACGACACTTGCTAGCGTTGGCGGTGCTTCA	685		
DB	323	CCAACTTACTCTCCCTGGGCTGTCAACGATGACCTTGCTTACGCTTTCGTGTGTAACAAGA	382		
QY	686	TTTCTGTGTGTAACGAAGCTACTTGTGTGTGCTGTTTTCAGATCAATTCACCTCTGA	745		
DB	383	TCCTCCGGTGTGCTCCAGGCGACAGCTGATGTGTGCTGTGCTATGCTTGAACCTTCAACATG	442		

Qy	746	CTGGCGCAAGGTAAGATGGTGTTCAGTAACCAACACATGGTTCTACCTGGCT	805
Db	443	GCCCCGTMAAGGCAAGATGATGTCCTCAGTCCACCAACATCTGAGATATCTCGCG	502
Qy	806	CTAACACTGGTGTCTCACTTTGACTTGCACATATGCCCGGTGTGTGTTCATCTACATG	865
Db	503	ACAAC-----CACTTCGATCTCATGATGACCCGGGGGTGTCCGATCTTTCGACG	553
Qy	866	GTGTGGCACTCAATAGGGGTCTCCACCCAGATGTTGGGGTGCAAGATACGGCGGTGTT	925
Db	554	GCTGCACCTCTGAATTTGG-----CAAGCTCTGGGGGTGCCAGATACGGCGGTATCT	607
Qy	926	CTTTCGCTCTGACTGTTCTTACCTTCTCTTGTGCCCTTCAAGCTGTTGTGAATGAGAT	985
Db	608	CCTCCCGAAGGAAATGATATGCTACCCCGAGCTTCTCAAGAGACGGTTGCCACTGGCGAT	667
Qy	986	TCGGCTGTTCAAAAACGCTGATATACCCACCATAGACTATACAAACAGTTACTGTCCCA	1045
Db	668	TCGACTGGTTTGAGAGAGCGCGACAACCTGACTTACCTTTGAGAGAGTTCAAGTCCCA	727
Qy	1046	AGGCTATCTACTCCCAATCTGGCTG	1070
Db	728	AGGCTCTCTCGACATCAGTGGATG	752

LOCUS	BD002249	1473 bp	DNA	linear	PAT 31-JAN-2002
DEFINITION	Cellulase preparation comprising endoglucanase.				
ACCESSION	BD002249				
VERSION	BD002249.1 GI:18630210				
KEYWORDS	JP 2000217583-A/2.				
SOURCE	Fusarium oxysporum.				
ORGANISM	Fusarium oxysporum. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.				
REFERENCE	1 (bases 1 to 1473) Gurete,R., Moller,M.J., Martin,S. and Ananto,P.S. Cellulase preparation comprising endoglucanase Patent: JP 2000217583-A 2 08-AUG-2000; NOVO NORDISK A/S				
AUTHORS	OS Fusarium oxysporum				
TITLE	PN JP 2000217583-A/2				
JOURNAL	PD 08-AUG-2000				
COMMENT	PF 22-DEC-1999 JP 1999365341 PR 09-MAY-1990 DK 1159/90 22-APR-1991 DK 0736/91 PI RASMUSSEN GURETE, MIKKELSEN JEN MOLLER, SCHEIN MARTIN, PI PATUL SHAMKANTO ANANTO PC C12N15/09, C11D3/386, C12N1/15, C12N1/19, C12N9/42, C12S3/04, PC D06M16/00// PP D21H11/20, (C12N9/42, C12R1:645), C12N15/00 CC FH Key Location/Qualifiers FT CDS (97)..(1224).				
FEATURES	source 1..1473 /organism="Fusarium oxysporum" /db_xref="taxon:5507"				
BASE COUNT	343 a 453 c 337 g 340 t				
ORIGIN					
Query Match	20.1%; Score 218.2; DB 6; Length 1473;				
Best Local Similarity	63.0%; Pred. No. 1e-48;				
Matches 394; Conservative	0; Mismatches 213; Indels 18; Gaps 3				
449	GTGTGCTCCGCTGAATGCTGAACCACTGCTCTGGAGTTGTTGAAGCTTCTTCA 508				
143	GTGTGCTTCTGGAAGCGGTCACTTACTTCATATGAGATTGCTCAAGCTTCTTGT 202				
509	GTTGGCCCGTAAAGCTGATGTCACCTCCCTGTTGGCTCTCTGTAAACAGATGGTAA 568				

Db	203	CTTGGAGGGAAAGGCTGTCGACAGCCCTCTTATCTTGATGATMAAGCAACAC	262
Qy	569	CTCTTGTGATTAACAACACTMAAAAGGGCTGT---GTGGGGATAGAGGTACACCTGA	625
Db	263	CCATTTCCAAACAACATAGCTGTGCACAGGTGTATAGAGGTGTGTCTTGCTTATGCTTCA	322
Qy	626	ATGACATCAACTTGGGTTGTATAGCGACACTTGGCTAGGGTTTGGCGGTCTGTCCA	685
Db	323	CCAACTACTCTCCCTGGGTGTGCACATATAGCTTGTCTTAAGGTTTGCTGTCAACAGA	382
Qy	686	TTTCTGSGTGTAGCGAAGCTACTTGTGTGTGTGTCCTGTTCGAACTCAATTCACCTTA	745
Db	383	TCTCCGGGTGCTCCGAGGCGACGCTGGTGTGTGTCTTGTGATATGCTTATACCTTACACAGC	442
Qy	746	CTGCGCTCAAGGGTATAGAGATGTGTGTTCAATATACAACTAGTGTTCGACTTGGCT	805
Db	443	GCCCGGTCAAGGGCAAGAAAGATGATGTGTCGATTCACAACTAGAGAGTGTCTGGGG	502
Qy	806	CTAACACTGGTGTCACTTTGATCTTGCAAATAGCCGGGTGGGTGTGGATCTTAATAG	865
Db	503	ACAAAC-----CACTTGCATCTCATGATGCCGGGTGTGTGTGTGGATCTTTCGAG	553
Qy	866	GTGTGCGCACTCAATGGGGTGTCTCCCAACCGATGGTGGGGTGTGCAAGATACGGCGGT	925
Db	554	GCTGCACCTCTGAGTTGCG-----CAAGGCTCTCGGGCGGTGCCAGATAGCGGGATCT	607
Qy	926	CTTGTGCTCTGACTGTCTTAACCTTCTCTGCGCCCTCAACACTGGTGTGATGTAGAT	985
Db	608	CTCCCGAAGGATGTGATAGCTAACCCCGACGGCTTCTCAAGACAGGTGTGCACCTGCGCAT	667
Qy	986	TGCGGTGGTTCAAAAAGCGGTATATACCAACCAATGACTATCAAAACAAGTATACCTGTCCA	1045
Db	668	TGCACTGTGTGAGAAAGCGCGACCAACCTGTACTCACTTTAGAGAGTTCAATGCCCA	727
Qy	1046	AGGCTATATCTGCCAAGTGTGGCTG	1070
Db	728	AGGCTTCTCTCGACATCAAGTGATG	752

LOCUS	BD010853	RESULT 12
DEFINITION	BD010853	
VERSION	BD010853.1	
KEYWORDS	JP 2001057894-A/2.	
SOURCE	Fusarium oxysporum	
ORGANISM	Fusarium oxysporum	
REFERENCE	1 (bases 1 to 1473)	
AUTHORS	Rasmussen,G., Mikkelsen,J.M., Schilein,M., Packar,S.A., Hagen,F., Miland,H.K. and Halstropu,S.	
TITLE	Cellulase preparation containing endoglucanase	
JOURNAL	Patent: JP 2001057894-A 2 06-MAR-2001;	
COMMENT	NOVO NORDISK AS	
OS	Fusarium oxysporum	
PN	JP 2001057894-A/2	
PD	06-MAR-2001	
PF	06-JUL-2000 JP 2000205757	
PR	09-MAY-1990 DK 1159/90, 22-APR-1991 DK 0736/91 PI	
GU	RETE RASMUSSEN, JAN MOLLER MIKKELSEN, MARTIN SCHILEIN, PI	
SH	SHAKUNT ANANT PATKAR, FRED HAGEN, HOERT KARSTEN MILAND, PI	
HALSTROP	SVEND	
PC	CI2N15/09 CI1D3/386 CI2N1/15 CI2N1/19 CI2N9/24 D06M16/00// PC	
PC	(CI2N15/09, CI2R1:77), (CI2N15/09, CI2R1:645), (CI2N9/24, PC	
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PC	(CI2N9/24, CI2R1:685), (CI2N15/00, (CI2N15/00, CI2R1:77),	
CC	(CI2N15/00, PC CI2R1:645)	
CC		
Key		
Location/Qualifiers		

FEATURES	FT	CDS	97	.1224
source		Location/Qualifiers		
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		/organism="Fusarium oxysporum"		
		/db_xref="taxon:5507"		
BASE COUNT		343	a	453
ORIGIN			c	337
			g	340
			t	

	Query Match	Similarity	20.1%;	Score 218.2;	DB 6;	Length 1473;
	Best Local	Similarity	63.0%;	Pred. No.1e-48;		
	Matches	394;	Conservative	0;	Mismatches 213;	Indels 18; Gaps 3
Qy	449	GTGTGGCTCCGGTAAATGTGTGAACCACTGGCACTGGATGGGATTTGTTGAAGCGCTTTGCA	508			
Db	143	GTGCTGCTTTGGAAGCGGTCACTCACTCAATACGGAATTCGTGCACAGCTTTCTTGGT	202			
Qy	509	GTTGCCCGGGTAAGGTGATGTCACCTCCCTGTTGGCTTCGTACAAAGATGATGA	568			
Db	203	CTTGAGACGGAAAGGTGTGTGTCAACGCGCTCTTTAACTGTGATAGAACACAAACC	262			
Qy	569	CTTCTGTGATTAACAACATCAAAAGCGGTGT--GTGTGTGTAGAGCTACCTGT	625			
Db	263	CCATTTTCAACACCAATGTGTCAACAGTGTGTAGGGTGTGTGTCTGTGCTTGA	322			
Qy	626	ATGCAATCAACCTTGATGTTGTAGCAACACCTTGCACTGTTTGGCGCTGCTTCA	685			
Db	323	CCAACTCACTCCCTGGGTGTCAACAGTGAAGTTCCTACAGTTTCGCTGTACAAAG	382			
Qy	686	TTTCTGAGGTATACGAAGCTATCTTGAGTGTGTGTCTGTTTCGAATCAATCACTCTTA	745			
Db	383	TCTCGGTGGCTCCGAGCGAGCTGTGTGTGTCTGTGATCTTTGACTTTGACCACTG	442			
Qy	746	CTGCGCTCAAGGTAAGAAAGATGTTGTTCAATAATACCAACCTGGTTCGACCTTGGCT	805			
Db	443	GCCCGGTAAAGGCAAGAAAGATGATCGTCAAGTCCACCAACTGTGAAGTAACTCGGG	502			
Qy	806	GTAAACACTGTGTCACTTTGACTTGCAATGCCCGGTGTGTGTGTGTGTATCTACAA	865			
Db	503	ACAAAC-----CACTTCGATCTCAATGATGCCCGAGTGTGTGTGTGTGTCTTGAGG	553			
Qy	866	GTTTGTGCACCTCAATGGGTGTCTCCACCAAGATGGTGTGGGTGTCAAGATACGGCGGT	925			
Db	554	GCTGACCTCTGAGTTGCG-----CAAGGCTCTGCGCGGTGTCCCAAGTACGGCGATCTC	607			
Qy	926	CTTGTGCTCTGACTGTTTCTAACCTTCCTTCTGCGCTCAACTGTGTGTGAATGAGAT	985			
Db	608	CTCTCCGAAGCATGTGTATGACTACCCCGGAGCTTCTCAAGACAGGTGTGCACATGGAGAT	667			
Qy	986	TGCGGTGTTCAAAAAGCTGTAAACCAACCAACATGACTTAAACAAATCTACGTGCCA	1041			
Db	668	TGTACTGTGTGAAAGCGCGACCAACCTGACTTCACTTTAGAGAGTTCAATGAGCCCA	727			
Qy	1046	AGGCTATCACTGCGCAAGTGTGGTG	1070			
Db	728	AGGCTCTCTCGACATCAATGGAATG	752			

RESULT 13			
LOCUS	113885	1473 bp	DNA
DEFINITION	Sequence 3 from patent US 5443750.		
ACCESSION	113885		
VERSION	113885.1	GI:996365	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1473)		
TITLE	Convents A., Baech A. and Baech A.C.		
JOURNAL	Detergent compositions with high activity cellulase and softening		
FEATURES	clysbs Patent: US 5443750-A 3 22-AUG-1995;		
	Location/Qualifiers		

source 1.1473
/organism="unknown"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

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Oy 449 GTGTCCTCCGATATGTAAGTAAACCTGCTACTGAGATTTGTAAGCTTCTTGA 508
Db 143 GTGTCCTCTCGAAGCGGTACTCTACTGATCTGGATTTGCAAGCTTCTTGTCT 202
Oy 509 GTTGCCCGGTAAGGCTGATGTCACTCCCTGTTGGCTCCCTGTAACAAGATGTAGA 568
Db 203 CTGGAAGCGAAGAGGCTGCTCAAGCCCTGCTTTAACTTGTGATGAAGACAAACC 262
Oy 569 CTCTTGCTGATTAACAACCTCAAAACGGCTGT---GTTGTGTAGACACTACCTGTA 625
Db 263 CCAATTCACACCAACATGCTGTCAACGGTTGAGGGGTGTGTTCTGCTTATGCTTGA 322
Oy 626 ATGACATCAACCTTGGTTTGAACGACCTTGGCTTACGTTTGGCGCTGCTTCCA 685
Db 323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTTACGTTTCCGCTCAACA 382
Oy 686 TTTCTGCTGATGAGGAGCTACTTGGTGTGCTGCTGTTGGAAGTCACTTCACTTCA 745
Db 383 TCTCCGGTGTCCGAGGCGACGCTGTGTGCTGTGCTTGAAGCTTCACTTCACTG 442
Oy 746 CTGCGCTCAAGGATTAAGATGTTGTTCAAGTAACAACACTGTGTTCTGACCTTGGCT 805
Db 443 GCCCGTCAAGGAGGAGAGATGATGTCGATCCACCAACATGAGATGATCTCGGCG 502
Oy 806 CTAAACCTGTGCTCACTTGAATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 865
Db 503 ACAAC-----CACTTCGATCTCATGATGCCGCGGTGTGTGTGTGTGTGTGTGTGT 553
Oy 866 GTTGTCACATCAATGGGGGTGCTCCACGATGTTGGGTGCAAGATGAGCGGCTGTTT 925
Db 554 GCTGACCTCTGAGTTGG-----CAAGGCTCTCGGCGGTGCGCAAGTACCGGATCT 607
Oy 926 CTTCGCTCTGACTGTTCTAACCTTCTTCCCTTCAAGCTGTGTGTGTGTGTGTGTGT 985
Db 608 CTTCCCGAAGGATGTATGATAGCTACCCGAGCTTCTCAAGAGCGTTGCCATGCGGAT 667
Oy 986 TCGGCTGTCAAAAACCTGATTAACCAACATGATCTTCAACAAGTAACTGTGCCA 1045
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Oy 1046 AGGCTATCATGCGCAAGCTGCGCTG 1070
Db 728 AGGCTCTCTCGACATCATGAGATG 752
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RESULT 14
LOCUS 121317 1473 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 3 from patent US 5520838.
ACCESSION 121317
VERSION 121317.1 GI:1601671
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

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Oy 449 GTGTCCTCCGATATGTAAGTAAACCTGCTACTGAGATTTGTAAGCTTCTTGA 508
Db 143 GTGTCCTCTCGAAGCGGTACTCTACTGATCTGGATTTGCAAGCTTCTTGTCT 202
Oy 509 GTTGCCCGGTAAGGCTGATGTCACTCCCTGTTGGCTCCCTGTAACAAGATGTAGA 568
Db 203 CTGGAAGCGAAGAGGCTGCTCAAGCCCTGCTTTAACTTGTGATGAAGACAAACC 262
Oy 569 CTCTTGCTGATTAACAACCTCAAAACGGCTGT---GTTGTGTAGACACTACCTGTA 625
Db 263 CCAATTCACACCAACATGCTGTCAACGGTTGAGGGGTGTGTTCTGCTTATGCTTGA 322
Oy 626 ATGACATCAACCTTGGTTTGAACGACCTTGGCTTACGTTTGGCGCTGCTTCCA 685
Db 323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTTACGTTTCCGCTCAACA 382
Oy 686 TTTCTGCTGATGAGGAGCTACTTGGTGTGCTGCTGTTTGAAGTCACTTCACTTCA 745
Db 383 TCTCCGGTGTCCGAGGCGACGCTGTGTGCTGTGCTTGAAGCTTCACTTCACTG 442
Oy 746 CTGCGCTCAAGGATTAAGATGTTGTTCAAGTAACAACACTGTGTTCTGACCTTGGCT 805
Db 443 GCCCGTCAAGGAGGAGAGATGATGTCGATCCACCAACATGAGATGATCTCGGCG 502
Oy 806 CTAAACCTGTGCTCACTTGAATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 865
Db 503 ACAAC-----CACTTCGATCTCATGATGCCGCGGTGTGTGTGTGTGTGTGTGTGT 553
Oy 866 GTTGTCACATCAATGGGGGTGCTCCACGATGTTGGGTGCAAGATGAGCGGCTGTTT 925
Db 554 GCTGACCTCTGAGTTGG-----CAAGGCTCTCGGCGGTGCGCAAGTACCGGATCT 607
Oy 926 CTTCGCTCTGACTGTTCTAACCTTCTTCCCTTCAAGCTGTGTGTGTGTGTGTGTGT 985
Db 608 CTTCCCGAAGGATGTATGATAGCTACCCGAGCTTCTCAAGAGCGTTGCCATGCGGAT 667
Oy 986 TCGGCTGTCAAAAACCTGATTAACCAACATGATCTTCAACAAGTAACTGTGCCA 1045
Db 668 TCGACTGTGTGAGAACCGCAACCTGACTTCACTTGAAGAGGTTGAGTGGCCCA 727
Oy 1046 AGGCTATCATGCGCAAGCTGCGCTG 1070
Db 728 AGGCTCTCTCGACATCATGAGATG 752
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RESULT 15
LOCUS 157984 1473 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5610129.
ACCESSION 157984
VERSION 157984.1 GI:2483048
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

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DB 143 GTGCTGCTCTTGGAAGCCGATCACTCTCATGATATGAGGATGCTGCAAGCCTTCTTGCT 202
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DB 203 CTTGAGACGGAAGGCTGCTGTCAACGCCCTGCTTAACTTGATTAAGAAACAACACC 262
OY 569 CTCTTGCTATATACAACTCAAAAAGGCTGT---GTTGGTGTAGACAGCTACACCTGTA 625
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OY 626 ATGACATATCAACTTGGGTTGTATGACGACGACTTGCTACGGTTTCCGCGCTTGCA 685
DB 323 CCAACTATCTCCCTGGGCTGTCAACGATGAGCTTACGCTTTCGCTGTACCAAGA 382
OY 686 TTTCTGTGTAGCGAAGCTACTGTGTGTGCTGTCTGTTCGAACTCAATTCACTCTTA 745
DB 383 TCTCCGATGCTCCGAGGCGAGCTGTGTGTGTGTGTATGCTTGAACCTTCAACACTG 442
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DB 503 ACAAC-----CACTTCATCTCATGATGCCGCGGTGTGTGTGTGTGTGTGTGTGT 553
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DB 554 GCTGCACTCTGATGTGCG-----CAAGGCTCTCGCGGTGTGCGCAATACGCGGTATCT 607
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DB 728 AGGCTCTCCGCAATCAAGTGTGATG 752
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